



SEQUENCE LISTING

<110> CORY, SUZANNE
ADAMS, JERRY
HUANG, DAVID C.S.
O'CONNOR, LIAM
STRASSER, ANDREAS
PUTHALAKATH, HAMSA
O'REILLY, LORRAINE

RECEIVED

OCT 17 2001

TECH CENTER 1600/2900

<120> NOVEL THERAPEUTIC MOLECULES

<130> 017227/0159

<140> 09/508,832

<141> 2000-07-10

<150> PCT/AU98/00772

<151> 1998-09-17

<150> AU PO 9263

<151> 1997-09-17

<150> AU PO 9373

<151> 1997-09-24

<160> 39

<170> PatentIn Ver. 2.1

<210> 1

<211> 332

<212> DNA

<213> Mus sp.

<220>

<221> CDS

<222> (1)..(330)

<400> 1

atg gcc aag caa cct tct gat gta agt tct gag tgt gac aga gaa ggt 48
Met Ala Lys Gln Pro Ser Asp Val Ser Ser Glu Cys Asp Arg Glu Gly
1 5 10 15

gga caa ttg cag cct gct gag agg cct ccc cag ctg agg cct ggg gcc 96
Gly Gln Leu Gln Pro Ala Glu Arg Pro Pro Gln Leu Arg Pro Gly Ala
20 25 30

cct acc tcc cta cag aca gaa ccg caa gct tcc ata cga cag tct cag 144
Pro Thr Ser Leu Gln Thr Glu Pro Gln Ala Ser Ile Arg Gln Ser Gln
35 40 45

gag gaa cct gaa gat ctg cgc ccg gag ata cgg att gca cag gag ctg 192
Glu Glu Pro Glu Asp Leu Arg Pro Glu Ile Arg Ile Ala Gln Glu Leu
50 55 60

cgg cgg atc gga gac gag ttc aac gaa act tac aca agg agg gtg ttt 240
 Arg Arg Ile Gly Asp Glu Phe Asn Glu Thr Tyr Thr Arg Arg Val Phe
 65 70 75 80

gca aat gat tac cgc gag gct gaa gac cac cct caa atg gtt atc tta 288
 Ala Asn Asp Tyr Arg Glu Ala Glu Asp His Pro Gln Met Val Ile Leu
 85 90 95

caa ctg tta cgc ttt atc ttc cgt ctg gta tgg aga agg cat tg 332
 Gln Leu Leu Arg Phe Ile Phe Arg Leu Val Trp Arg Arg His
 100 105 110

<210> 2
 <211> 110
 <212> PRT
 <213> Mus sp.

<400> 2
 Met Ala Lys Gln Pro Ser Asp Val Ser Ser Glu Cys Asp Arg Glu Gly
 1 5 10 15

Gly Gln Leu Gln Pro Ala Glu Arg Pro Pro Gln Leu Arg Pro Gly Ala
 20 25 30

Pro Thr Ser Leu Gln Thr Glu Pro Gln Ala Ser Ile Arg Gln Ser Gln
 35 40 45

Glu Glu Pro Glu Asp Leu Arg Pro Glu Ile Arg Ile Ala Gln Glu Leu
 50 55 60

Arg Arg Ile Gly Asp Glu Phe Asn Glu Thr Tyr Thr Arg Arg Val Phe
 65 70 75 80

Ala Asn Asp Tyr Arg Glu Ala Glu Asp His Pro Gln Met Val Ile Leu
 85 90 95

Gln Leu Leu Arg Phe Ile Phe Arg Leu Val Trp Arg Arg His
 100 105 110

<210> 3
 <211> 422
 <212> DNA
 <213> Mus sp.

<220>
 <221> CDS
 <222> (1)..(420)

<400> 3
 atg gcc aag caa cct tct gat gta agt tct gag tgt gac aga gaa ggt 48
 Met Ala Lys Gln Pro Ser Asp Val Ser Ser Glu Cys Asp Arg Glu Gly
 1 5 10 15

gga caa ttg cag cct gct gag agg cct ccc cag ctc agg cct ggg gcc 96
 Gly Gln Leu Gln Pro Ala Glu Arg Pro Pro Gln Leu Arg Pro Gly Ala
 20 25 30

B2
 wt

<210> 4
<211> 140
<212> PRT
<213> Mus sp.

```

<400> 4
Met Ala Lys Gln Pro Ser Asp Val Ser Ser Glu Cys Asp Arg Glu Gly
  1          5          10          15
Gly Gln Leu Gln Pro Ala Glu Arg Pro Pro Gln Leu Arg Pro Gly Ala
  20          25          30
Pro Thr Ser Leu Gln Thr Glu Pro Gln Asp Arg Ser Pro Ala Pro Met
  35          40          45
Ser Cys Asp Lys Ser Thr Gln Thr Pro Ser Pro Pro Cys Gln Ala Phe
  50          55          60
Asn His Tyr Leu Ser Ala Met Ala Ser Ile Arg Gln Ser Gln Glu Glu
  65          70          75          80
Pro Glu Asp Leu Arg Pro Glu Ile Arg Ile Ala Gln Glu Leu Arg Arg
  85          90          95
Ile Gly Asp Glu Phe Asn Glu Thr Tyr Thr Arg Arg Val Phe Ala Asn
  100          105          110

```

Asp Tyr Arg Glu Ala Glu Asp His Pro Gln Met Val Ile Leu Gln Leu
115 120 125

Leu Arg Phe Ile Phe Arg Leu Val Trp Arg Arg His
130 135 140

<210> 5
<211> 590
<212> DNA
<213> Mus sp.

<220>
<221> CDS
<222> (1)..(588)

<400> 5
atg gcc aag caa cct tct gat gta agt tct gag tgt gac aga gaa ggt 48
Met Ala Lys Gln Pro Ser Asp Val Ser Ser Glu Cys Asp Arg Glu Gly
1 5 10 15

gga caa ttg cag cct gct gag agg cct ccc cag ctg agg cct ggg gcc 96
Gly Gln Leu Gln Pro Ala Glu Arg Pro Pro Gln Leu Arg Pro Gly Ala
20 25 30

cct acc tcc cta cag aca gaa ccg caa ggt aat ccc gac ggc gaa ggg 144
Pro Thr Ser Leu Gln Thr Glu Pro Gln Gly Asn Pro Asp Gly Glu Gly
35 40 45

gac cgc tgc ccc cac ggc agc cct cag ggc ccg ctg gcc cca ccg gcc 192
Asp Arg Cys Pro His Gly Ser Pro Gln Gly Pro Leu Ala Pro Pro Ala
50 55 60

agc cct ggc cct ttt gct acc aga tcc cca ctt ttc atc ttt gtg aga 240
Ser Pro Gly Pro Phe Ala Thr Arg Ser Pro Leu Phe Ile Phe Val Arg
65 70 75 80

aga tct tct ctg ctg tcc cgg tcc tcc agt ggg tat ttc tct ttt gac 288
Arg Ser Ser Leu Leu Ser Arg Ser Ser Ser Gly Tyr Phe Ser Phe Asp
85 90 95

aca gac agg agc ccg gca ccc atg agt tgt gac aag tca aca caa acc 336
Thr Asp Arg Ser Pro Ala Pro Met Ser Cys Asp Lys Ser Thr Gln Thr
100 105 110

cca agt cct cct tgc cag gcc ttc aac cac tat ctg agt gca atg gct 384
Pro Ser Pro Pro Cys Gln Ala Phe Asn His Tyr Leu Ser Ala Met Ala
115 120 125

tcc ata cga cag tct cag gag gaa cct gaa gat ctg cgc ccg gag ata 432
Ser Ile Arg Gln Ser Gln Glu Glu Pro Glu Asp Leu Arg Pro Glu Ile
130 135 140

cgg att gca cag gag ctg cgg cgg atc gga gac gag ttc aac gaa act 480
Arg Ile Ala Gln Glu Leu Arg Arg Ile Gly Asp Glu Phe Asn Glu Thr
145 150 155 160

tac aca agg agg gtg ttt gca aat gat tac cgc gag gct gaa gac cac 528
Tyr Thr Arg Arg Val Phe Ala Asn Asp Tyr Arg Glu Ala Glu Asp His
165 170 175

cct caa atg gtt atc tta caa ctg tta cgc ttt atc ttc cgt ctg gta 576
Pro Gln Met Val Ile Leu Gln Leu Leu Arg Phe Ile Phe Arg Leu Val
180 185 190

tgg aga agg cat tg 590
Trp Arg Arg His
195

<210> 6
<211> 196
<212> PRT
<213> Mus sp.

<400> 6
Met Ala Lys Gln Pro Ser Asp Val Ser Ser Glu Cys Asp Arg Glu Gly
1 5 10 15

Gly Gln Leu Gln Pro Ala Glu Arg Pro Pro Gln Leu Arg Pro Gly Ala
20 25 30

Pro Thr Ser Leu Gln Thr Glu Pro Gln Gly Asn Pro Asp Gly Glu Gly
35 40 45

Asp Arg Cys Pro His Gly Ser Pro Gln Gly Pro Leu Ala Pro Pro Ala
50 55 60

Ser Pro Gly Pro Phe Ala Thr Arg Ser Pro Leu Phe Ile Phe Val Arg
65 70 75 80

Arg Ser Ser Leu Leu Ser Arg Ser Ser Ser Gly Tyr Phe Ser Phe Asp
85 90 95

Thr Asp Arg Ser Pro Ala Pro Met Ser Cys Asp Lys Ser Thr Gln Thr
100 105 110

Pro Ser Pro Pro Cys Gln Ala Phe Asn His Tyr Leu Ser Ala Met Ala
115 120 125

Ser Ile Arg Gln Ser Gln Glu Glu Pro Glu Asp Leu Arg Pro Glu Ile
130 135 140

Arg Ile Ala Gln Glu Leu Arg Arg Ile Gly Asp Glu Phe Asn Glu Thr
145 150 155 160

Tyr Thr Arg Arg Val Phe Ala Asn Asp Tyr Arg Glu Ala Glu Asp His
165 170 175

Pro Gln Met Val Ile Leu Gln Leu Leu Arg Phe Ile Phe Arg Leu Val
180 185 190

Trp Arg Arg His
195

<210> 7
 <211> 416
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(414)

<400> 7
 atg gca aag caa cct tct gat gta agt tct gag tgt gac cga gaa ggt 48
 Met Ala Lys Gln Pro Ser Asp Val Ser Ser Glu Cys Asp Arg Glu Gly
 1 5 10 15

aga caa ttg cag cct gcg gag agg cct ccc cag ctc aga cct ggg gcc 96
 Arg Gln Leu Gln Pro Ala Glu Arg Pro Pro Gln Leu Arg Pro Gly Ala
 20 25 30

cct acc tcc cta cag aca gag cca caa gac agg agc cca gca ccc atg 144
 Pro Thr Ser Leu Gln Thr Glu Pro Gln Asp Arg Ser Pro Ala Pro Met
 35 40 45

agt tgt gac aaa tca aca caa acc cca agt cct cct tgc cag gcc ttc 192
 Ser Cys Asp Lys Ser Thr Gln Thr Pro Ser Pro Pro Cys Gln Ala Phe
 50 55 60

aac cac tat ctc agt gca atg gct tcc atg agg cag gct gaa cct gca 240
 Asn His Tyr Leu Ser Ala Met Ala Ser Met Arg Gln Ala Glu Pro Ala
 65 70 75 80

gat atg cgc cca gag ata tgg atc gcc caa gag ttg cgg cgt atc gga 288
 Asp Met Arg Pro Glu Ile Trp Ile Ala Gln Glu Leu Arg Arg Ile Gly
 85 90 95

gac gag ttt aac gct tac tat gca agg agg gta ttt ttg aat aat tac 336
 Asp Glu Phe Asn Ala Tyr Tyr Ala Arg Arg Val Phe Leu Asn Asn Tyr
 100 105 110

caa gca gcc gaa gac cac cca cga atg gtt atc tta cga ctg tta cgt 384
 Gln Ala Ala Glu Asp His Pro Arg Met Val Ile Leu Arg Leu Leu Arg
 115 120 125

tac att gtc cgc ctg gtg tgg aga atg cat tg 416
 Tyr Ile Val Arg Leu Val Trp Arg Met His
 130 135

<210> 8
 <211> 138
 <212> PRT
 <213> Homo sapiens

<400> 8
 Met Ala Lys Gln Pro Ser Asp Val Ser Ser Glu Cys Asp Arg Glu Gly
 1 5 10 15

Arg Gln Leu Gln Pro Ala Glu Arg Pro Pro Gln Leu Arg Pro Gly Ala
 20 25 30

Pro Thr Ser Leu Gln Thr Glu Pro Gln Asp Arg Ser Pro Ala Pro Met
 35 40 45

Ser Cys Asp Lys Ser Thr Gln Thr Pro Ser Pro Pro Cys Gln Ala Phe
 50 55 60

Asn His Tyr Leu Ser Ala Met Ala Ser Met Arg Gln Ala Glu Pro Ala
 65 70 75 80

Asp Met Arg Pro Glu Ile Trp Ile Ala Gln Glu Leu Arg Arg Ile Gly
 85 90 95

Asp Glu Phe Asn Ala Tyr Tyr Ala Arg Arg Val Phe Leu Asn Asn Tyr
 100 105 110

Gln Ala Ala Glu Asp His Pro Arg Met Val Ile Leu Arg Leu Leu Arg
 115 120 125

Tyr Ile Val Arg Leu Val Trp Arg Met His
 130 135

<210> 9
 <211> 596
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(594)

atg gca aag caa cct tct gat gta agt tct gag tgt gac cga gaa ggt 48
 Met Ala Lys Gln Pro Ser Asp Val Ser Ser Glu Cys Asp Arg Glu Gly
 1 5 10 15

aga caa ttg cag cct gcg gag agg cct ccc cag ctc aga cct ggg gcc 96
 Arg Gln Leu Gln Pro Ala Glu Arg Pro Pro Gln Leu Arg Pro Gly Ala
 20 25 30

cct acc tcc cta cag aca gag cca caa ggt aat cct gaa ggc aat cac 144
 Pro Thr Ser Leu Gln Thr Glu Pro Gln Gly Asn Pro Glu Gly Asn His
 35 40 45

gga ggt gaa ggg gac agc tgc ccc cac ggc agc cct cag ggc ccg ctg 192
 Gly Gly Glu Gly Asp Ser Cys Pro His Gly Ser Pro Gln Gly Pro Leu
 50 55 60

gcc cca cct gcc agc cct ggc cct ttt gct acc aga tcc ccg ctt ttc 240
 Ala Pro Pro Ala Ser Pro Gly Pro Phe Ala Thr Arg Ser Pro Leu Phe
 65 70 75 80

atc ttt atg aga aga tcc tcc ctg ctg tct cga tcc tcc agt ggg tat 288
 Ile Phe Met Arg Arg Ser Ser Leu Leu Ser Arg Ser Ser Ser Gly Tyr
 85 90 95

ttc tct ttt gac aca gac agg agc cca gca ccc atg agt tgt gac aaa	336
Phe Ser Phe Asp Thr Asp Arg Ser Pro Ala Pro Met Ser Cys Asp Lys	
100 105 110	
tca aca caa acc cca agt cct cct tgc cag gcc ttc aac cac tat ctc	384
Ser Thr Gln Thr Pro Ser Pro Pro Cys Gln Ala Phe Asn His Tyr Leu	
115 120 125	
agt gca atg gct tcc atg agg cag gct gaa cct gca gat atg cgc cca	432
Ser Ala Met Ala Ser Met Arg Gln Ala Glu Pro Ala Asp Met Arg Pro	
130 135 140	
gag ata tgg atc gcc caa gag ttg cgg cgt atc gga gac gag ttt aac	480
Glu Ile Trp Ile Ala Gln Glu Leu Arg Arg Ile Gly Asp Glu Phe Asn	
145 150 155 160	
gct tac tat gca agg agg gta ttt ttg aat aat tac caa gca gcc gaa	528
Ala Tyr Tyr Ala Arg Arg Val Phe Leu Asn Asn Tyr Gln Ala Ala Glu	
165 170 175	
gac cac cca cga atg gtt atc tta cga ctg tta cgt tac att gtc cgc	576
Asp His Pro Arg Met Val Ile Leu Arg Leu Leu Arg Tyr Ile Val Arg	
180 185 190	
ctg gtg tgg aga atg cat tg	596
Leu Val Trp Arg Met His	
195	

<210> 10
 <211> 198
 <212> PRT
 <213> Homo sapiens

<400> 10
 Met Ala Lys Gln Pro Ser Asp Val Ser Ser Glu Cys Asp Arg Glu Gly
 1 5 10 15
 Arg Gln Leu Gln Pro Ala Glu Arg Pro Pro Gln Leu Arg Pro Gly Ala
 20 25 30
 Pro Thr Ser Leu Gln Thr Glu Pro Gln Gly Asn Pro Glu Gly Asn His
 35 40 45
 Gly Gly Glu Gly Asp Ser Cys Pro His Gly Ser Pro Gln Gly Pro Leu
 50 55 60
 Ala Pro Pro Ala Ser Pro Gly Pro Phe Ala Thr Arg Ser Pro Leu Phe
 65 70 75 80
 Ile Phe Met Arg Arg Ser Ser Leu Leu Ser Arg Ser Ser Ser Gly Tyr
 85 90 95
 Phe Ser Phe Asp Thr Asp Arg Ser Pro Ala Pro Met Ser Cys Asp Lys
 100 105 110

Ser Thr Gln Thr Pro Ser Pro Pro Cys Gln Ala Phe Asn His Tyr Leu
 115 120 125

Ser Ala Met Ala Ser Met Arg Gln Ala Glu Pro Ala Asp Met Arg Pro
 130 135 140

Glu Ile Trp Ile Ala Gln Glu Leu Arg Arg Ile Gly Asp Glu Phe Asn
 145 150 155 160

Ala Tyr Tyr Ala Arg Arg Val Phe Leu Asn Asn Tyr Gln Ala Ala Glu
 165 170 175

Asp His Pro Arg Met Val Ile Leu Arg Leu Leu Arg Tyr Ile Val Arg
 180 185 190

Leu Val Trp Arg Met His
 195

<210> 11
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 11
 Asp Tyr Lys Asp Asp Asp Asp Lys
 1 5

<210> 12
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 12
 Glu Tyr Met Pro Met Glu
 1 5

<210> 13
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 13
 Leu Arg Arg Ile Gly Asp Glu
 1 5

<210> 14
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 14
 tgggagaaca gggtagatcg atgcggg

27

<210> 15
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 15
 gtgaactggg agcggattgt gg

22

BR
W
 <210> 16
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 16
 cacctgcaca ccgcatcca ggataacg

28

<210> 17
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 17
 aggatccacc atggccaagc aacc

24

<210> 18
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 18

gttctagatc agcacatctc tctgggatag aaccac

36

<210> 19

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 19

gcaagcttcc tgtgcaatcc gtatctcc

28

<210> 20

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 20

ggaagcttgc aacgaaactt acacaaggtg

30

<210> 21

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 21

gcaagcttcc gggcgagat cttc

24

<210> 22

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 22

caaagcttcc tgtgcaatcc gtatctcc

28

<210> 23

<211> 30

<212> DNA

BD
W

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 23

ggaagctttg aacgaaactt acacaaggtg

30

<210> 24

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 24

caaagcttcc gggcgagat cttc

24

<210> 25

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 25

taagttctga gtgtgacaga gaaggtgg

28

<210> 26

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 26

cagttgtaag ataaccattt gaggggtgg

28

<210> 27

<211> 18

<212> PRT

<213> Homo sapiens

<400> 27

Val Val His Leu Thr Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg
1 5 10 15

Tyr Arg

<210> 28

<211> 18
 <212> PRT
 <213> Homo sapiens

<400> 28
 Ala Val Lys Gln Ala Leu Arg Glu Ala Gly Asp Glu Phe Glu Leu Arg
 1 5 10 15

Tyr Arg

<210> 29
 <211> 18
 <212> PRT
 <213> Homo sapiens

<400> 29
 Pro Leu His Gln Ala Met Arg Ala Ala Gly Asp Glu Phe Glu Thr Arg
 1 5 10 15

Phe Arg

<210> 30
 <211> 18
 <212> PRT
 <213> Homo sapiens

<400> 30
 Lys Ala Leu Glu Thr Leu Arg Arg Val Gly Asp Gly Val Gln Arg Asn
 1 5 10 15

His Glu

<210> 31
 <211> 18
 <212> PRT
 <213> Homo sapiens

<400> 31
 Lys Leu Ser Glu Cys Leu Lys Arg Ile Gly Asp Glu Leu Asp Ser Asn
 1 5 10 15

Met Glu

<210> 32
 <211> 18
 <212> PRT
 <213> Homo sapiens

<400> 32
 Gln Val Gly Arg Gln Leu Ala Ile Ile Gly Asp Asp Ile Asn Arg Arg
 1 5 10 15

Tyr Asp

<210> 33
 <211> 18
 <212> PRT
 <213> Homo sapiens

<400> 33
 Arg Tyr Gly Arg Glu Leu Arg Arg Met Ser Asp Glu Phe Val Asp Ser
 1 5 10 15


Phe Lys

<210> 34
 <211> 18
 <212> PRT
 <213> Homo sapiens

<400> 34
 Ala Leu Ala Leu Arg Leu Ala Cys Ile Gly Asp Glu Met Asp Val Ser
 1 5 10 15

Leu Arg

<210> 35
 <211> 18
 <212> PRT
 <213> Homo sapiens

 <400> 35
 Asn Ile Ala Arg His Leu Ala Gln Val Gly Asp Ser Met Asp Arg Ser
 1 5 10 15

Ile Pro

<210> 36
 <211> 18
 <212> PRT
 <213> Homo sapiens

<400> 36
 Leu Thr Ala Ala Arg Leu Lys Ala Leu Gly Asp Glu Leu His Gln Arg
 1 5 10 15

Thr Met

<210> 37
 <211> 18
 <212> PRT
 <213> Homo sapiens

<400> 37
 Trp Ile Ala Gln Glu Leu Arg Arg Ile Gly Asp Glu Phe Asn Ala Tyr
 1 5 10 15

Tyr Ala

<210> 38
 <211> 20
 <212> PRT
 <213> Homo sapiens

<400> 38
 Met Arg Pro Glu Ile Trp Ile Ala Gln Glu Leu Arg Arg Ile Gly Asp
 1 5 10 15

Glu Phe Asn Ala
 20

<210> 39
 <211> 20
 <212> PRT
 <213> Caenorhabditis elegans

<400> 39
 Gln Glu Glu Thr Ile Arg Trp Ala Gln Glu Leu Arg Leu Arg Cys Leu
 1 5 10 15

Val Thr Thr Arg
 20